

## WEST Search History

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DATE: Wednesday, August 16, 2006

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L8	L7 not l6	55
<input type="checkbox"/>	L7	L3 and kidney	189
<input type="checkbox"/>	L6	l2 and (autoimmune or lupus or sle)	152
<input type="checkbox"/>	L5	L4 and l1	1
<input type="checkbox"/>	L4	L2 same (autoimmune or lupus or sle)	1
<input type="checkbox"/>	L3	l2 and (array or microarray or profile)	227
<input type="checkbox"/>	L2	L1 same (expression or mRNA)	308
<input type="checkbox"/>	L1	SFRP1 or FRP or SARP2 or (secreted adj (apoptosis or frizzled) adj related adj protein)	18257

END OF SEARCH HISTORY

## Myers, Carla

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SYSTEM:OS - DIALOG OneSearch

- File 5:Biosis Previews(R) 1969-2006/Aug W1  
(c) 2006 The Thomson Corporation
- File 6:NTIS 1964-2006/Aug W1  
(c) 2006 NTIS, Intl Cpyrght All Rights Res
- File 8:Ei Compendex(R) 1970-2006/Aug W1  
(c) 2006 Elsevier Eng. Info. Inc.
- File 24:CSA Life Sciences Abstracts 1966-2006/Jun  
(c) 2006 CSA.
- File 34:SciSearch(R) Cited Ref Sci 1990-2006/Aug W1  
(c) 2006 The Thomson Corp
- File 45:EMCare 2006/Aug W1  
(c) 2006 Elsevier B.V.
- File 65:Inside Conferences 1993-2006/Aug 16  
(c) 2006 BLDSC all rts. reserv.
- File 71:ELSEVIER BIOBASE 1994-2006/Aug W2  
(c) 2006 Elsevier B.V.
- File 73:EMBASE 1974-2006/Aug 16  
(c) 2006 Elsevier B.V.
- File 94:JICST-EPlus 1985-2006/May W1  
(c) 2006 Japan Science and Tech Corp(JST)
- File 98:General Sci Abs 1984-2005/Jan  
(c) 2006 The HW Wilson Co.
- File 99:Wilson Appl. Sci & Tech Abs 1983-2006/Jul  
(c) 2006 The HW Wilson Co.
- File 135:NewsRx Weekly Reports 1995-2006/Aug W1  
(c) 2006 NewsRx
- File 136:BioEngineering Abstracts 1966-2006/Jul  
(c) 2006 CSA.
- File 143:Biol. & Agric. Index 1983-2006/Jul  
(c) 2006 The HW Wilson Co
- File 144:Pascal 1973-2006/Jul W4  
(c) 2006 INIST/CNRS
- File 155:MEDLINE(R) 1950-2006/Aug 15  
(c) format only 2006 Dialog
- File 172:EMBASE Alert 2006/Aug 16  
(c) 2006 Elsevier B.V.
- File 266:FEDRIP 2005/Dec  
Comp & dist by NTIS, Intl Copyright All Rights Res
- File 315:ChemEng & Biotec Abs 1970-2006/Jul  
(c) 2006 DECHEMA
- File 357:Derwent Biotech Res. \_1982-2006/Aug W2  
(c) 2006 The Thomson Corp.
- File 358:Current BioTech Abs 1983-2006/Jan  
(c) 2006 DECHEMA
- File 369:New Scientist 1994-2006/Jul W3  
(c) 2006 Reed Business Information Ltd.
- File 370:Science 1996-1999/Jul W3  
(c) 1999 AAAS

\*File 370: This file is closed (no updates). Use File 47 for more current information.

File 399:CA SEARCH(R) 1967-2006/UD=14508  
(c) 2006 American Chemical Society

\*File 399: Use is subject to the terms of your user/customer agreement.  
IPCR/8 classification codes now searchable as IC=. See HELP NEWSIPCR.

Set Items Description

? s SFRP1 or (secreted (w) frizzle\$ (w) related (w) protein) or SARP2 or SFRP-1  
555 SFRP1  
328608 SECRETED  
0 FRIZZLE\$  
7877444 RELATED  
10289834 PROTEIN  
0 SECRETED(W)FRIZZLE\$(W)RELATED(W)PROTEIN  
41 SARP2  
33 SFRP-1  
S1 627 SFRP1 OR (SECRETED (W) FRIZZLE\$ (W) RELATED (W) PROTEIN)  
OR SARP2 OR SFRP-1

? s SFRP1 or (secreted (w) frizzled (w) related (w) protein) or SARP2 or SFRP-1  
Processing

Processed 20 of 26 files ...

Completed processing all files

555 SFRP1  
328608 SECRETED  
6916 FRIZZLED  
7877444 RELATED  
10289834 PROTEIN  
1027 SECRETED(W)FRIZZLED(W)RELATED(W)PROTEIN  
41 SARP2  
33 SFRP-1  
S2 1377 SFRP1 OR (SECRETED (W) FRIZZLED (W) RELATED (W) PROTEIN)  
OR SARP2 OR SFRP-1

s s2 and (autoimmune or lupus or sle or RA or rheumatoid)

1377 S2  
491380 AUTOIMMUNE  
271377 LUPUS  
78024 SLE  
617272 RA  
422382 RHEUMATOID  
S3 42 S2 AND (AUTOIMMUNE OR LUPUS OR SLE OR RA OR RHEUMATOID)

? rd s3

S4 17 RD S3 (unique items)

? s s2 and (expression or mRNA or profile)

1377 S2  
6020558 EXPRESSION  
1391965 mRNA  
1135906 PROFILE

S5 1015 S2 AND (EXPRESSION OR mRNA OR PROFILE)

? s s5 and (array or microarray)

1015 S5  
584443 ARRAY  
164260 MICROARRAY

S6 188 S5 AND (ARRAY OR MICROARRAY)

? rd s6

S7 84 RD S6 (unique items)

? s s7 not s3

84 S7  
42 S3

S8 80 S7 NOT S3t s10/6/1-38

Run on: August 3, 2006, 10:58:55 ; Search time 24395 Seconds  
(without alignments)  
11714.738 Million cell updates/sec

Title: US-10-786-720-15  
Perfect score: 4469  
Sequence: 1 cctgcagcctccggagttag.....taatcaatgaaaaaaaaaa 4469

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
1	4469	100.0	4469	2	CS025753		CS025753 Sequence
2	4469	100.0	4469	2	AX236302		AX236302 Sequence
3	4469	100.0	4469	2	AX578081		AX578081 Sequence
4	4469	100.0	4469	5	AF056087		AF056087 Homo sapi
5	4356.8	97.5	4500	2	AR253209		AR253209 Sequence
6	4339.4	97.1	4482	5	BC036503		BC036503 Homo sapi
7	3935	88.1	4245	2	AR129158		AR129158 Sequence
8	3580.6	80.1	3670	2	BD135188		BD135188 Human nuc
9	3580.6	80.1	3670	2	AX017498		AX017498 Sequence
10	3504.8	78.4	3872	2	CQ850220		CQ850220 Sequence
11	3504.8	78.4	3872	5	AK127331		AK127331 Homo sapi
12	3448	77.2	171133	5	AC103846		AC103846 Homo sapi
13	3448	77.2	188270	5	AC104393		AC104393 Homo sapi

14	3081	68.9	3181	2	BD205077	BD205077 Human nuc	
15	3081	68.9	3181	2	AX013686	AX013686 Sequence	
16	2465.4	55.2	2602	2	AX099741	AX099741 Sequence	
17	2075	46.4	2075	2	AR253206	AR253206 Sequence	
18	2075	46.4	2075	2	AR361924	AR361924 Sequence	
19	2075	46.4	2075	2	AR433000	AR433000 Sequence	
20	2075	46.4	2075	2	AX482567	AX482567 Sequence	
21	2075	46.4	2075	2	AX565707	AX565707 Sequence	
22	2075	46.4	2075	2	AX597107	AX597107 Sequence	
23	2075	46.4	2075	2	AX701365	AX701365 Sequence	
24	2075	46.4	2075	5	AF001900	AF001900 Homo sapi	
25	2062	46.1	2078	2	AR253205	AR253205 Sequence	
26	1991.6	44.6	2094	5	AF017987	AF017987 Homo sapi	
27	1476.6	33.0	4240	14	BTU85945	U85945 Bos taurus	
28	1256.6	28.1	1308	2	BD217906	BD217906 Gene fami	
29	1196.8	26.8	4375	6	BC094662	BC094662 Mus muscu	
30	923.8	20.7	945	8	AY891055	AY891055 Synthetic	
31	923.8	20.7	945	8	BT019677	BT019677 Synthetic	
c	32	906.4	20.3	197427	12	AC182062	AC182062 Bos tauru
	33	899.8	20.1	942	2	AR361925	AR361925 Sequence
	34	899.8	20.1	942	2	AX482568	AX482568 Sequence
	35	896.8	20.1	1017	2	AR361926	AR361926 Sequence
	36	896.2	20.1	1340	6	BC024495	BC024495 Mus muscu
	37	886.4	19.8	2659	6	MMU88566	U88566 Mus musculu
	38	828.2	18.5	155691	5	AC016868	AC016868 Homo sapi
	39	776.2	17.4	2124	2	AR253208	AR253208 Sequence
	40	703.6	15.7	3065	11	GGA404652	AJ404652 Gallus ga
	41	684.2	15.3	804	2	AR361929	AR361929 Sequence
	42	621.2	13.9	741	2	AR361928	AR361928 Sequence
	43	609.6	13.6	1146	2	AX565729	AX565729 Sequence
	44	609.6	13.6	1146	2	AX597129	AX597129 Sequence
	45	609.6	13.6	1146	2	AX701375	AX701375 Sequence
	46	609.4	13.6	770	5	HSA325301	AJ325301 Homo sapi
	47	609	13.6	726	7	BV208829	BV208829 SFRP1_189
c	48	588	13.2	241809	6	AC139848	AC139848 Mus muscu
c	49	536	12.0	184377	6	AC147247	AC147247 Mus muscu
c	50	527	11.8	548	2	AR280573	AR280573 Sequence

Run on: August 3, 2006, 10:56:23 ; Search time 2549 Seconds  
(without alignments)  
12224.001 Million cell updates/sec

Title: US-10-786-720-15  
Perfect score: 4469  
Sequence: 1 cctqcaqcctccggagtcag.....taatcaatqaaaaaaaaaa 4469

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## **SUMMARIES**

8

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	4469	100.0	4469	4	AAS12954		Aas12954 Human Fri
2	4469	100.0	4469	6	ABT10165		Abt10165 Human bre
3	4469	100.0	4469	8	ABZ34845		Abz34845 Coding se
4	4469	100.0	4469	12	ADP21417		Adp21417 Gene SFRP
5	4469	100.0	4469	13	ADR24996		Adr24996 Breast ca
6	4469	100.0	4469	13	ADR99015		Adr99015 Secreted
7	4469	100.0	4469	13	AEA64538		Aea64538 Human lup
8	4469	100.0	4469	14	ADV44809		Adv44809 Secreted
9	4469	100.0	4469	14	ADX58915		Adx58915 Human reg
C 10	4439.8	99.3	4608	14	AED73309		Aed73309 Human pla
11	4393.4	98.3	4462	8	ABX77526		Abx77526 Different
12	4355.4	97.5	4616	4	AAH72901		Aah72901 Human cer
13	4355.2	97.5	4497	2	AAV84395		Aav84395 Human Fri

14	4335.4	97.0	4451	8	ABZ82226	Abz82226 Human sFR
15	3935	88.1	4245	4	AAF80506	Aaf80506 Cell prol
16	3580.6	80.1	3670	2	AAZ33577	Aaz33577 Human bre
17	3504.8	78.4	3872	13	ADR07183	Adr07183 Full leng
18	3102.6	69.4	3215	3	AAC77657	Aac77657 Human can
19	3090.4	69.2	3216	2	AAZ33608	Aaz33608 Human bre
20	3069	68.7	3180	2	AAZ42127	Aaz42127 Human nor
21	2465.4	55.2	2602	12	ADP68535	Adp68535 Human sec
22	2075	46.4	2075	4	AAD17401	Aad17401 Human sec
23	2075	46.4	2075	6	ABV73022	Abv73022 Human sec
24	2075	46.4	2075	8	ABX75330	Abx75330 Human cDN
25	2075	46.4	2075	8	AAD52558	Aad52558 FRP DNA.
26	2075	46.4	2075	12	ADH43319	Adh43319 Human sec
27	2074.6	46.4	2075	10	ADC71197	Adc71197 Human sec
28	2059	46.1	2072	8	ABZ81830	Abz81830 Receptor
29	1991.6	44.6	2094	8	ABZ82228	Abz82228 Human sec
30	1256.6	28.1	1308	2	AAV19115	Aav19115 Human sec
c	31	978.6	21.9	1247	13 ACN41451	Acn41451 Human dia
	32	942	21.1	942	8 ABZ82227	Abz82227 Human sec
	33	942	21.1	942	9 ACC81035	Acc81035 Human emb
	34	899.8	20.1	942	6 ABV73023	Abv73023 Human sec
	35	899.8	20.1	942	10 ADC71198	Adc71198 ORF of th
	36	899.8	20.1	942	12 ADH43320	Adh43320 Human sec
	37	896.8	20.1	1017	10 ADC71192	Adc71192 DNA encod
	38	896.8	20.1	1017	12 ADH43314	Adh43314 Human sFR
	39	812.2	18.2	945	9 ACC81034	Acc81034 Murine em
	40	800.8	17.9	2124	2 AAV84394	Aav84394 Partial F
	41	684.2	15.3	804	10 ADC71195	Adc71195 DNA encod
	42	684.2	15.3	804	12 ADH43317	Adh43317 Human sec
	43	621.2	13.9	741	10 ADC71194	Adc71194 DNA encod
	44	621.2	13.9	741	12 ADH43316	Adh43316 Human sec
	45	609.6	13.6	1146	8 ABX75340	Abx75340 Human cDN
	46	609.6	13.6	1146	8 AAD52570	Aad52570 SRFP 1 DN
	47	609.6	13.6	1146	8 ABZ81842	Abz81842 WIF-1 nuc
	48	551.8	12.3	566	14 ACL62743	Acl62743 Human col
c	49	527	11.8	548	4 AAF17593	Aaf17593 Human bre
c	50	527	11.8	548	4 AAS47023	Aas47023 Human bre

Run on: August 3, 2006, 11:01:00 ; Search time 765 Seconds  
(without alignments)  
10930.700 Million cell updates/sec

Title: US-10-786-720-15  
Perfect score: 4469  
Sequence: 1 cctgcagcctccggagttag.....taatcaatgaaaaaaaaaa 4469

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : Issued\_Patents\_NA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

၁၆

Result	Query						Description	
No.	Score	Match	Length	DB	ID			
1	4469	100.0	4469	3	US-09-949-016-428		Sequence 428, App	
2	4469	100.0	4469	5	US-09-796-008-1		Sequence 1, Appli	
3	4356.8	97.5	4500	3	US-09-087-031E-27		Sequence 27, Appli	
4	3935	88.1	4245	3	US-09-276-531-16		Sequence 16, Appli	
5	3258.8	72.9	7360	3	US-09-949-016-15054		Sequence 15054, A	
6	3258.4	72.9	3360	3	US-09-949-016-3312		Sequence 3312, Ap	
7	2075	46.4	2075	3	US-09-087-031E-2		Sequence 2, Appli	
8	2075	46.4	2075	3	US-09-546-043-1		Sequence 1, Appli	
9	2075	46.4	2075	3	US-09-514-885-2		Sequence 2, Appli	
10	2062	46.1	2078	3	US-09-087-031E-1		Sequence 1, Appli	
11	1256.6	28.1	1308	3	US-08-937-067-18		Sequence 18, Appli	
12	899.8	20.1	942	3	US-09-546-043-2		Sequence 2, Appli	
13	896.8	20.1	1017	3	US-09-546-043-9		Sequence 9, Appli	
14	776.2	17.4	2124	3	US-09-087-031E-26		Sequence 26, Appli	
15	684.2	15.3	804	3	US-09-546-043-12		Sequence 12, Appli	
16	621.2	13.9	741	3	US-09-546-043-11		Sequence 11, Appli	
c	17	600.6	13.4	601	3	US-09-949-016-26352		Sequence 26352, A
c	18	600.6	13.4	601	3	US-09-949-016-119368		Sequence 119368,

c	19	597.4	13.4	601	3	US-09-949-016-26353	Sequence 26353, A
c	20	597.4	13.4	601	3	US-09-949-016-119369	Sequence 119369,
c	21	587	13.1	601	3	US-09-949-016-26354	Sequence 26354, A
c	22	587	13.1	601	3	US-09-949-016-119370	Sequence 119370,
c	23	579.6	13.0	601	3	US-09-949-016-26355	Sequence 26355, A
c	24	579.6	13.0	601	3	US-09-949-016-119371	Sequence 119371,
c	25	527	11.8	548	3	US-09-222-575-78	Sequence 78, Appl
c	26	527	11.8	548	3	US-09-389-681-78	Sequence 78, Appl
c	27	527	11.8	548	3	US-09-620-405B-78	Sequence 78, Appl
c	28	527	11.8	548	3	US-09-339-338-78	Sequence 78, Appl
c	29	527	11.8	548	3	US-09-433-826B-78	Sequence 78, Appl
c	30	527	11.8	548	3	US-09-604-287A-78	Sequence 78, Appl
c	31	527	11.8	548	3	US-09-285-480-78	Sequence 78, Appl
c	32	527	11.8	548	3	US-09-834-759-78	Sequence 78, Appl
c	33	527	11.8	548	3	US-09-590-751A-78	Sequence 78, Appl
c	34	527	11.8	548	3	US-09-551-621-78	Sequence 78, Appl
c	35	527	11.8	548	3	US-09-551-621A-78	Sequence 78, Appl
c	36	527	11.8	548	3	US-10-076-622-78	Sequence 78, Appl
c	37	527	11.8	548	4	US-10-124-805-78	Sequence 78, Appl
	38	468.8	10.5	588	3	US-09-546-043-10	Sequence 10, Appl
	39	444	9.9	690	3	US-09-546-043-13	Sequence 13, Appl
	40	400	9.0	1984	3	US-08-937-067-5	Sequence 5, Appli
	41	399.2	8.9	1905	3	US-09-949-016-429	Sequence 429, App
	42	393.4	8.8	1719	3	US-09-949-016-1835	Sequence 1835, Ap
c	43	320	7.2	601	3	US-09-949-016-26356	Sequence 26356, A
c	44	320	7.2	601	3	US-09-949-016-119372	Sequence 119372,
	45	253.2	5.7	9086	3	US-09-949-016-13577	Sequence 13577, A
	46	253.2	5.7	85369	3	US-09-949-016-12171	Sequence 12171, A
	47	238.4	5.3	240	5	US-09-796-008-3	Sequence 3, Appli
	48	233.6	5.2	2030	3	US-08-937-067-1	Sequence 1, Appli
	49	224.8	5.0	2027	5	US-08-949-904A-1	Sequence 1, Appli
	50	223.4	5.0	1869	3	US-09-148-545-56	Sequence 56, Appl

Run on: August 3, 2006, 11:09:19 ; Search time 4965 Seconds  
(without alignments)  
11060.109 Million cell updates/sec

Title: US-10-786-720-15

Perfect score: 4469

Sequence: 1 cctgcaqgcctccggagtcag.....taatcaatqaaaaaaaaaa 4469

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

## **Database :**

### Published Applications NA Main:\*

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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

96

Result	Query						Description
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	1	4469	100.0	4469	3	US-09-796-008-1	Sequence 1, Appli
	2	4469	100.0	4469	7	US-10-133-937-42	Sequence 42, Appl
	3	4469	100.0	4469	7	US-10-172-118-857	Sequence 857, App
	4	4469	100.0	4469	7	US-10-159-563-42	Sequence 42, Appl
	5	4469	100.0	4469	8	US-10-342-887-857	Sequence 857, App
	6	4469	100.0	4469	9	US-10-786-720-15	Sequence 15, Appl
	7	4469	100.0	4469	9	US-10-788-792-21	Sequence 21, Appl
	8	4469	100.0	4469	9	US-10-473-974-203	Sequence 203, App
	9	4469	100.0	4469	9	US-10-817-525-1	Sequence 1, Appli
	10	4469	100.0	4469	16	US-11-245-147-203	Sequence 203, App
c	11	4439.8	99.3	4608	10	US-10-821-234-137	Sequence 137, App
	12	4393.4	98.3	4462	3	US-09-974-298-28	Sequence 28, Appl

13	4356.8	97.5	4500	7	US-10-138-434A-27	Sequence 27, Appl	
14	3102.6	69.4	3215	3	US-09-925-301-51	Sequence 51, Appl	
15	2465.4	55.2	2602	8	US-10-666-851-1	Sequence 1, Appl	
16	2075	46.4	2075	7	US-10-138-434A-2	Sequence 2, Appl	
17	2075	46.4	2075	7	US-10-425-586-1	Sequence 1, Appl	
18	2075	46.4	2075	8	US-10-466-136-1	Sequence 1, Appl	
19	2062	46.1	2078	7	US-10-138-434A-1	Sequence 1, Appl	
20	1991.6	44.6	2094	10	US-10-756-149-3306	Sequence 3306, Ap	
21	1256.6	28.1	1308	6	US-10-146-474-18	Sequence 18, Appl	
22	1256.6	28.1	1308	8	US-10-301-764-18	Sequence 18, Appl	
23	899.8	20.1	942	7	US-10-425-586-2	Sequence 2, Appl	
24	899.8	20.1	942	8	US-10-466-136-2	Sequence 2, Appl	
25	896.8	20.1	1017	7	US-10-425-586-9	Sequence 9, Appl	
26	776.2	17.4	2124	7	US-10-138-434A-26	Sequence 26, Appl	
27	684.2	15.3	804	7	US-10-425-586-12	Sequence 12, Appl	
28	621.2	13.9	741	7	US-10-425-586-11	Sequence 11, Appl	
29	571.4	12.8	630	12	US-10-301-480-560598	Sequence 560598,	
30	571.4	12.8	630	12	US-10-301-480-1174007	Sequence 1174007,	
c	31	527	11.8	548	3	US-09-604-287A-78	Sequence 78, Appl
c	32	527	11.8	548	3	US-09-834-759-78	Sequence 78, Appl
c	33	527	11.8	548	3	US-09-339-338-78	Sequence 78, Appl
c	34	527	11.8	548	3	US-09-551-621-78	Sequence 78, Appl
c	35	527	11.8	548	6	US-10-007-805-78	Sequence 78, Appl
c	36	527	11.8	548	6	US-10-076-622-78	Sequence 78, Appl
c	37	527	11.8	548	7	US-10-124-805-78	Sequence 78, Appl
c	38	527	11.8	548	7	US-10-441-893-78	Sequence 78, Appl
c	39	527	11.8	548	16	US-11-226-869-78	Sequence 78, Appl
40	497	11.1	549	6	US-10-027-632-93316	Sequence 93316, A	
41	497	11.1	549	6	US-10-027-632-305035	Sequence 305035,	
42	497	11.1	549	7	US-10-027-632-93316	Sequence 93316, A	
43	497	11.1	549	7	US-10-027-632-305035	Sequence 305035,	
c	44	482	10.8	501	3	US-09-954-531-885	Sequence 885, App
c	45	482	10.8	501	3	US-09-954-531-1298	Sequence 1298, Ap
c	46	482	10.8	501	10	US-10-843-641A-1952	Sequence 1952, Ap
c	47	482	10.8	501	10	US-10-843-641A-2365	Sequence 2365, Ap
48	468.8	10.5	588	7	US-10-425-586-10	Sequence 10, Appl	
49	444	9.9	690	7	US-10-425-586-13	Sequence 13, Appl	
50	427.6	9.6	445	8	US-10-242-535A-43352	Sequence 43352, A	

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(without alignments)  
12876.977 Million cell updates/sec

Title: US-10-786-720-15  
Perfect score: 4469  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Minimum DB seq length: 0

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%

Listing first 150 summaries

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gb_gss2:*
gb_gss3:*
gb_gss4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	2	898	20.1	919	6	CR613872	CR613872 full-leng
	3	894.8	20.0	919	4	BX343566	BX343566 BX343566
	4	891	19.9	2704	6	AK088868	AK088868 Mus muscu
	5	887.6	19.9	918	1	AL528023	AL528023 AL528023
	6	845.6	18.9	887	4	BX402193	BX402193 BX402193
	7	821.8	18.4	911	5	CD519089	CD519089 AGENCOURT
	8	815.6	18.3	908	1	AU125245	AU125245 AU125245
	9	796.2	17.8	801	9	CX781693	CX781693 HESC3_8_B
	10	782.6	17.5	838	2	BG682306	BG682306 602629621
	11	780.8	17.5	891	8	CV810231	CV810231 AGENCOURT
	12	778.2	17.4	1011	3	BU196604	BU196604 AGENCOURT
	13	768	17.2	837	1	AU131621	AU131621 AU131621
	14	760.4	17.0	763	9	CX786676	CX786676 HESC3 63

15	759.8	17.0	785	9	CX781701	CX781701 HESC3_8_C
16	754.2	16.9	2298	6	AK081052	AK081052 Mus muscu
17	748.6	16.8	782	9	DA571541	DA571541 DA571541
c 18	748.6	16.8	886	1	AL528022	AL528022 AL528022
19	746	16.7	952	8	CO580514	CO580514 ILLUMIGEN
20	744.4	16.7	884	2	BG681605	BG681605 602628094
21	736.8	16.5	764	1	AU123839	AU123839 AU123839
22	736.8	16.5	814	5	CD644680	CD644680 AGENCOURT
23	732.8	16.4	913	3	BQ879583	BQ879583 AGENCOURT
c 24	727.8	16.3	803	5	CD616079	CD616079 56076764J
25	725.8	16.2	878	3	BQ876624	BQ876624 AGENCOURT
26	721.4	16.1	762	8	CN271890	CN271890 170004245
27	720.4	16.1	898	3	BQ680787	BQ680787 AGENCOURT
28	718.6	16.1	864	5	CD558546	CD558546 AGENCOURT
29	715.4	16.0	750	8	CN271875	CN271875 170005313
30	711	15.9	922	3	BQ932355	BQ932355 AGENCOURT
31	709.8	15.9	734	8	CN271881	CN271881 170006001
32	709.4	15.9	723	4	CA389569	CA389569 cs100d05.
33	708.6	15.9	762	1	AU125808	AU125808 AU125808
34	704.6	15.8	757	8	CN271867	CN271867 170005327
c 35	694.4	15.5	703	4	CA413793	CA413793 UI-H-EZ0-
c 36	693.8	15.5	701	4	CA313964	CA313964 UI-CF-FN0
c 37	689.2	15.4	701	3	BM670202	BM670202 UI-E-DW1-
38	681	15.2	823	1	AU127052	AU127052 AU127052
39	672.6	15.1	903	5	CD244905	CD244905 AGENCOURT
40	667.4	14.9	792	2	BG698901	BG698901 602703318
41	665	14.9	881	2	BG253035	BG253035 602365657
42	664.8	14.9	779	4	CB247875	CB247875 UI-M-FI0-
43	662.6	14.8	982	3	BU501489	BU501489 AGENCOURT
44	661.8	14.8	741	8	CR769220	CR769220 DKFZp469B
45	661.2	14.8	928	2	BG120117	BG120117 602353481
46	660	14.8	779	5	CD643855	CD643855 AGENCOURT
47	658.2	14.7	907	2	BG119546	BG119546 602347246
c 48	657.2	14.7	706	4	CA434170	CA434170 UI-H-DH0-
49	655.4	14.7	738	3	BQ771388	BQ771388 UI-M-FI0-
c 50	654.4	14.6	660	3	BM970588	BM970588 UI-CF-EC1